

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create ten species in the genus *Enamovirus (Sobelivirales:Solemoviridae)* |
| **Code assigned:** | 2025.020P.Solemoviridae\_Enamovirus\_10nsp | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses | **X** |
| Archaeal viruses |  | General |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
| *Solemoviridae* SG |

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| **Submission date:** | 16/06/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** |  |

**Part 3:** **TAXONOMIC PROPOSAL**

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *Enamovirus BUBEV* | Epithet from the virus name acronym |
| *Enamovirus CAEV* | Epithet from the virus name acronym |
| *Enamovirus CSEV* | Epithet from the virus name acronym |
| *Enamovirus CTEV* | Epithet from the virus name acronym |
| *Enamovirus DEGEV* | Epithet from the virus name acronym |
| *Enamovirus FTEV* | Epithet from the virus name acronym |
| *Enamovirus ORAEV* | Epithet from the virus name acronym |
| *Enamovirus RAEV* | Epithet from the virus name acronym |
| *Enamovirus WSEV* | Epithet from the virus name acronym |
| *Enamovirus YPEV* | Epithet from the virus name acronym |

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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Genus, species  *Description of current taxonomy*:  Currently, the genus *Enamovirus* consists of 15 species.  *Proposed* *taxonomic change(s):* Create ten new species in the genus *Enamovirus*  *Justification*: High-throughput sequencing (HTS) of raspberry samples collected in 2021 from Czechia and Norway has revealed 14 isolates of a novel *Enamovirus* candidate, raspberry enamovirus 1 (RaEV1). Carrot enamovirus 1 (CaEV1) was discovered in wild carrot populations in Southwestern France. In addition, the analyses of publicly available plant transcriptome data have enabled to assemble 16 additional genome sequences characteristic of *Enamovirus* species: brunioides conebush enamovirus, Bunge’s buttercup enamovirus, cassava enamovirus, common thyme enamovirus, Coriandrum sativum enamovirus, decurrent goldenrod enamovirus, Fukien tea tree enamovirus, oriental arborvitae enamovirus, rubber tree enamovirus, Rugel’s plantain enamovirus, sea-buckthorn enamo-like virus, showy sunflower enamovirus, silver birch enamovirus, spruce enamovirus, Western salsify enamovirus, and Yunnan pine enamovirus. Ten out of 18 candidate species are proposed as the new members of genus Enamovirus, fulfilling the species demarcation criteria and having complete or coding-complete genomes sequences. |

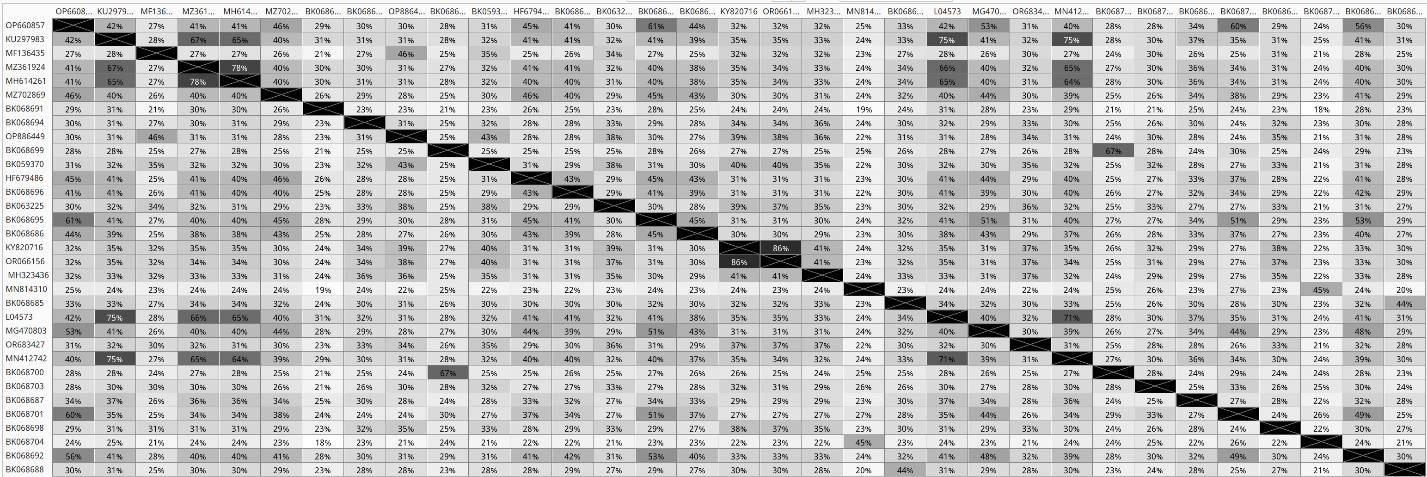
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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: Species  *Description of current taxonomy*: *Sobelivirales*:*Solemoviridae*:*Enamovirus*  *Proposed* *taxonomic change(s)*: Create ten new species.  *Demarcation criteria:*  The following species demarcation criteria for the genus *Enamovirus* were set in 2023 (accepted in 2024 by the ICTV):  • Differences in breadth and specificity of host range;  • Failure of cross-protection in either one-way or two-way relationships;  • Differences in serological specificity with discriminatory polyclonal or monoclonal antibodies;  • Differences in amino acid sequence identity of RdRPs >10%;  • Differences in nucleotide sequence identity of genomes around or >25%.  *Justification*:  Enamovirus genomes have five common major open reading frames (ORFs) designated as ORF0, 1, 2, 3, and 5. ORF0 encodes a viral RNA silencing suppressor protein (P0), ORF1 encodes the P1 protein, ORF2 encodes a viral RNA-directed RNA polymerase (RdRP; P2) which is involved in replication, ORF3 encodes the major coat protein (CP; P3), and ORF5 encodes an aphid-transmission factor (P5). The RdRP is synthesized by translational fusion with P1 (P1-P2) via a -1 ribosomal frameshift in ORF1. The P5 is expressed as a readthrough protein with P3 (P3-P5).  High-throughput sequencing (HTS) of raspberry (*Rubus idaeus*) samples collected in 2021 from Czechia and Norway has revealed 14 isolates of a novel *Enamovirus* candidate, **raspberry enamovirus 1 (RaEV1)** [1]. The RNA-Seq data was deposited in the NCBI SRA under BioProjectID PRJNA1028176. The genome sequence of the RaEV1 GR isolate (GenBank Acc. No. **OR683427**) was confirmed through Sanger sequencing and RACE procedures. The complete genome spans 5824 nucleotides. Five putative open reading frames (ORF0, ORF1, ORF2, ORF3, and ORF5) characteristic of enamoviruses were predicted. The pairwise comparisons of translated polymerase (RdRP) and coat protein (CP) observed the highest identity with the respective proteins encoded by Celmisia lyallii enamovirus RdRP (43%) and red clover enamovirus CP (33%), respectively (Table 1) **The recognition of RaEV1 as the member of the new species “*Enamovirus RAEV”* is consistent with the species demarcation criteria in the genus *Enamovirus.***  **Carrot enamovirus 1 (CaEV1)** was identified in wild carrot populations in the Southwest of France in 2019 [2].A nearly complete genome of CaEV1 was sequenced (**OP886449**). The genome organization of CaEV1 is typical for the genus, with five predicted ORFs. The sequence is most closely related to a partial sequence of Arracacha latent virus E (MF136435; Fig 4) with 57% aa identity and 56% nt identity in the full RdRp and the nearly full-length genome, respectively (Table 1). **The recognition of CaEV1 as the member of the new species “*Enamovirus CAEV”* is consistent with the species demarcation criteria in the genus *Enamovirus.***  In addition, the analyses of publicly available plant transcriptome data enabled the assembly of 16 additional genome sequences characteristic of *Enamovirus* species [3, 4]. The putative novel viruses identified in those libraries were tentatively regarded as viruses of the corresponding plant species. Eight of the identified enamoviruses corresponded to complete genomes and grouped with other known enamoviruses, and thus are proposed as members of new species (detailed below). Brunoides conebush enamovirus (BrcEV; BK068691) formed a separate subclade, and sea buckthorn enamo-like virus (SebEV; BK068687) grouped with poleroviruses in the RdRp- and CP-based phylogenies [3]. The genomes of cassava enamovirus (CasEV; BK068699), rubber tree enamovirus (RtEV; BK068700), Rugel's plantain enamovirus (RpEV; BK068703), showy sunflower enamovirus (SsEV; BK069701), silver birch enamovirus (SbEV; BK068698) and spruce enamovirus (SprEV; BK068704) are all partial, missing part of their 3' ends including the entire ORF5 [3]. SebEV also lacked the ORFs 3a and 4 characteristic of poleroviruses [3]. Thus, these 8 viruses cannot be recognized as species.  **Bunge's buttercup enamovirus (BubEV)** genome (**BK068694**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry SRR18512454 PRJNA820952) derived from *Ranunculus bungei* collected on the Qinghai-Tibet plateau, China [3]. The assembled near-complete genomic sequence spans 5261 nt. **The recognition of BubEV as member of the new species “*Enamovirus BUBEV*” is consistent with the species demarcation criteria in the genus *Enamovirus*.**  **Common thyme enamovirus (CtEV)** genome (**BK068696**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry SRR6262813; PRJNA417241) derived from the plants grown from the seeds of common thyme (*Thymus vulgaris*) collected around Saint Martin de Londres, 25 km north of Montpellier, France [3]. The assembled near-complete genomic sequence spans 6099 nt. **The recognition of CtEV as member of the species “*Enamovirus CtEV”* is consistent with the species demarcation criteria in genus *Enamovirus.***  **Coriandrum sativum enamovirus (CsEV)** genome was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry GGPN01011425; PRJNA472685) derived from coriander seeds grown in Rajasthan, India [4]. The assembled near-complete 5415-nt CsEV genome (GenBank Acc No **BK063225**) contained five ORFs characteristic of enamoviruses, encoding proteins P0, P1, P2, P3 and P5. Phylogenetic relationship of CsEV with other enamoviruses was confirmed based on viral coat protein (P3) amino acid sequence. **The recognition of CsEV as member of the new species “*Enamovirus CSEV”* is consistent with the species demarcation criteria in genus *Enamovirus.***  **Decurrent goldenrod enamovirus (DegEV)** genome (**BK068695**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry SRR5943633; PRJNA397809) derived from the plants sown from the seeds of decurrent goldenrod (*Solidago canadensis*) collected from a suburb of Wuhan city, China [3]. The assembled near-complete genomic sequence spans 5521 nt. **The recognition of DegEV as member of the new species “*Enamovirus DEGEV”* is consistent with the species demarcation criteria in genus *Enamovirus.***  **Fukien tea tree enamovirus (FtEV)** genome (GenBank Acc. No. **BK068686**) was assembled from the transcriptomice data (DDBJ/EMBL/GenBank entry SRR7076638; PRJNA454043) derived from the root sample of Fukien tea tree (*Ehretia microphylla*) collected in Nanjing, China [3]. The assembled near-complete genomic sequence spans 5992 nt. **The recognition of FtEV as member of the new species “*Enamovirus FTEV”* is consistent with the species demarcation criteria in genus *Enamovirus.***  **Oriental arborvitae enamovirus (OraEV)** genome (**BK068685**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry SRR5892426; PRJNA396655) derived from Chinese arborvitae (*Platycladus orientalis*) grown in the coniferous plant resource nursery at the Institute of Forestry and Pomology, Beijing, China [3]. The assembled near-complete genomic sequence spans 5768 nt. **The recognition of OraEV as member of the new species “*Enamovirus ORAEV”* is consistent with the species demarcation criteria in genus *Enamovirus.***  **Western salsify enamovirus (WsEV)** genome (**BK068692**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry SRR11802599; PRJNA633300) derived from yellow salsify (*Tragopogon dubius*) plants grown from field-collected seeds obtained at Moscow, Idaho, United States [3]. The assembled near-complete genomic sequence spans 5577 nt. **The recognition of WsEV as member of the new species“*Enamovirus WSEV”* is consistent with the species demarcation criteria in genus *Enamovirus.***  **Yunnan pine enamovirus (YpEV)** genome (**BK068688**) was assembled from the transcriptome data (DDBJ/EMBL/GenBank entry SRR9179537; PRJNA545862) derived from *Pinus yunnanensis* collected at Kunming, Yunnan, China [3]. The assembled near-complete genomic sequence spans 6221 nt. **The recognition of YpEV as member of the new species “*Enamovirus YPEV”* is consistent with the species demarcation criteria in genus *Enamovirus.***  Phylogenetic analysis of the putative enamovirus RdRP sequences supports the clustering of the ten new viruses within the genus Enamovirus (Fig. 1). |

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| **References:** |
| [1] Koloniuk I, Fránová J, Přibylová J, Sarkisova T, Špak J, Tan JL, Zemek R, Čmejla R, Rejlová M, Valentová L, Sedlák J, Holub J, Skalík J, Blystad DR, Sapkota B, Hamborg Z. Molecular Characterization of a Novel Enamovirus Infecting Raspberry. Viruses. 2023 Nov 21;15(12):2281. doi: 10.3390/v15122281.  [2] Schönegger D, Marais A, Babalola BM, Faure C, Lefebvre M, Svanella-Dumas L, Brázdová S, Candresse T. Carrot populations in France and Spain host a complex virome rich in previously uncharacterized viruses. PLoS One. 2023 Aug 16;18(8):e0290108. doi: 0.1371/journal.pone.0290108.  [3] Sidharthan VK, Reddy VP, Krishnan N, Parameswari B. Unveiling the genetic diversity of the genera *Enamovirus* and *Polerovirus* through data-driven virus discovery. Arch Virol. 2025 Mar 13;170(4):76. doi: 10.1007/s00705-025-06258-w.  [4] Kavi Sidharthan V, Diksha D, Singh R, Choudhary S, Naika MBN, Baranwal VK. Identification of two putative novel deltapartitiviruses and an enamovirus in coriander transcriptomes. Arch Microbiol. 2023 Sep 27;205(10):342. doi: 10.1007/s00203-023-03681-y. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.020P.N.v2.Solemoviridae\_Enamovirus\_10nsp.xlsx | Excel module |

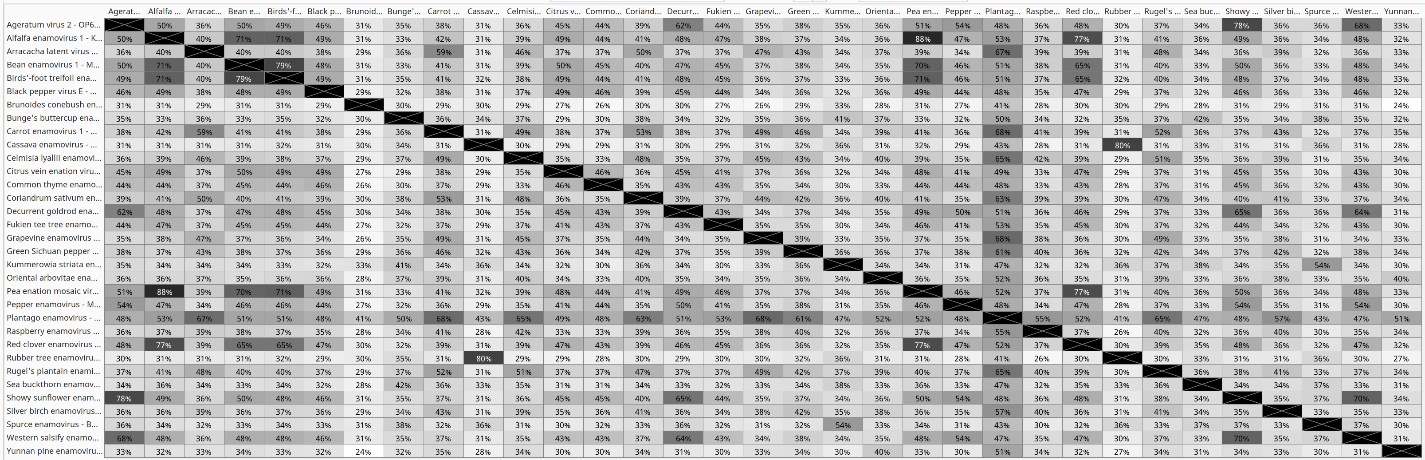
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| **Tables, Figures:** Table 1; Table 2; Fig. 1. |

**Table 1.** Percent identities between the nucleotide sequences of new and recognized\* enamovirus genomes retrieved from NCBI GenBank. Multiple sequence alignment was performed using the MUSCLE algorithm implemented in Geneious Prime ver. 2025.1.2.



\* OP660857 - Ageratum virus 2; KU297983 - Alfalfa enamovirus 1; MF136435 - Arracacha latent virus E; MZ361924 - bean enamovirus 1; MH614261 - bird's-foot trefoil enamovirus 1; MZ702869 - black pepper virus E; BK068691 - Brunioides conebush enamovirus; BK068694 - bunge's buttercup enamovirus; OP886449 – carrot enamovirus 1; BK068699 - cassava enamovirus; BK059370 - Celmisia lyallii enamovirus, HF679486 - Citrus vein enation virus; BK068696 - common thyme enamovirus; BK063225 - Coriandrum sativum enamovirus; BK068695 - Decurrent goldenrod enamovirus; BK068686 - Fukien tea tree enamovirus; KY820716 - Grapevine enamovirus 1; MH323436 - green Sichuan pepper enamovirus; MN814310 - Kummerowia striata enamovirus; BK068685 - oriental arborvitae enamovirus; L04573 - pea enation mosaic virus 1; MG470803 - pepper enamovirus; OR683427 - raspberry enamovirus 1; MN412742 - red clover enamovirus 1; BK068700 - rubber tree enamovirus; BK068703 - Rugel's plantain enamovirus; BK068687 - sea buckthorn enamo-like virus; BK068701 - showy sunflower enamovirus; BK068698 - silver birch enamovirus; BK068704 - spruce enamovirus; BK068692 - western salsify enamovirus; BK068688 - Yunnan pine enamovirus.

**Table 2.** Percent identities between amino acid sequences of new and recognized enamovirus RdRPs translated from ORF2 of exemplar isolate sequences (indicated in Table 1), starting at the ribosomal frameshift signal. Multiple sequence alignment was performed using the MUSCLE algorithm implemented in Geneious Prime ver. 2025.1.2.

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**Fig. 1. Phylogenetic analysis of RdRP amino acid sequences of poleroviruses and enamoviruses by the Maximum Likelihood method. RdRP of turnip rosette virus (TRoV, sobemovirus) was used as an outgroup. Putative new polerovirus sequences were marked with blue diamonds and putative new enamoviruses were marked with yellow diamonds. RdRPs grouping within enamovirus sequences were marked with rounded rectangle.**

The phylogeny was inferred using the Maximum Likelihood method and Le-Gascuel (2008) LG model (+Freq) of amino acid substitutions. The tree with the highest log likelihood (-71 207,36) is shown. The percentage of replicate trees in which the associated taxa clustered together, where the number of replicates (127) was determined adaptively, is shown. The initial tree for the heuristic search was selected by choosing the tree with the superior log-likelihood between a Neighbor-Joining (NJ) tree and a Maximum Parsimony (MP) tree. The NJ tree was generated using a matrix of pairwise distances computed using the Le-Gascuel (2008) LG model (+Freq). The MP tree had the shortest length among 10 MP tree searches, each performed with a randomly generated starting tree. The evolutionary rate differences among sites were modeled using a discrete Gamma distribution across 5 categories (+G, parameter = 0,4380), with 6,50% of sites deemed evolutionarily invariant (+I). The analytical procedure encompassed 130 amino acid sequences with 923 positions in the final dataset. Evolutionary analyses were conducted in MEGA12 (Kumar S., Stecher G., Suleski M., Sanderford M., Sharma S., and Tamura K. 2024. Molecular Evolutionary Genetics Analysis Version 12 for adaptive and green computing. Molecular Biology and Evolution 41:1-9).